

<120> ANTI-IL-20 ANTIBODIES AND BINDING
PARTNERS AND METHODS OF USING IN INFLAMMATION

cag cgg atc acc cgg aaq tcc tgc aac ctg acg gtg gag acg ggc aac 294

Gln	Arg	Ile	Thr	Arg	Lys	Ser	Cys	Asn	Leu	Thr	Val	Glu	Thr	Gly	Asn	
			75					80						85		
ctc	acg	gag	ctc	tac	tat	gcc	agg	gtc	acc	gct	gtc	agt	gcg	gga	ggc	342
Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val	Thr	Ala	Val	Ser	Ala	Gly	Gly	
		90					95					100				
cgg	tca	gcc	acc	aag	atg	act	gac	agg	ttc	agc	tct	ctg	cag	cac	act	390
Arg	Ser	Ala	Thr	Lys	Met	Thr	Asp	Arg	Phe	Ser	Ser	Leu	Gln	His	Thr	
	105					110					115					
acc	ctc	aag	cca	cct	gat	gtg	acc	tgt	atc	tcc	aaa	gtg	aga	tcg	att	438
Thr	Leu	Lys	Pro	Pro	Asp	Val	Thr	Cys	Ile	Ser	Lys	Val	Arg	Ser	Ile	
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Gln	Met	Ile	Val	His	Pro	Thr	Pro	Thr	Pro	Ile	Arg	Ala	Gly	Asp	Gly	
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cac	cgg	cta	acc	ctg	gaa	gac	atc	ttc	cat	gac	ctg	ttc	tac	cac	tta	534
His	Arg	Leu	Thr	Leu	Glu	Asp	Ile	Phe	His	Asp	Leu	Phe	Tyr	His	Leu	
			155					160					165			
gag	ctc	cag	gtc	aac	cgc	acc	tac	caa	atg	cac	ctt	gga	ggg	aag	cag	582
Glu	Leu	Gln	Val	Asn	Arg	Thr	Tyr	Gln	Met	His	Leu	Gly	Gly	Lys	Gln	
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Arg	Glu	Tyr	Glu	Phe	Phe	Gly	Leu	Thr	Pro	Asp	Thr	Glu	Phe	Leu	Gly	
	185					190					195					
acc	atc	atg	att	tgc	gtt	ccc	acc	tgg	gcc	aag	gag	agt	gcc	ccc	tac	678
Thr	Ile	Met	Ile	Cys	Val	Pro	Thr	Trp	Ala	Lys	Glu	Ser	Ala	Pro	Tyr	
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Met	Cys	Arg	Val	Lys	Thr	Leu	Pro	Asp	Arg	Thr	Trp	Thr	Tyr	Ser	Phe	
				220					225					230		
tcc	gga	gcc	ttc	ctg	ttc	tcc	atg	ggc	ttc	ctc	gtc	gca	gta	ctc	tgc	774
Ser	Gly	Ala	Phe	Leu	Phe	Ser	Met	Gly	Phe	Leu	Val	Ala	Val	Leu	Cys	
			235					240					245			
tac	ctg	agc	tac	aga	tat	gtc	acc	aag	ccg	cct	gca	cct	ccc	aac	tcc	822
Tyr	Leu	Ser	Tyr	Arg	Tyr	Val	Thr	Lys	Pro	Pro	Ala	Pro	Pro	Asn	Ser	
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ctg	aac	gtc	cag	cga	gtc	ctg	act	ttc	cag	ccg	ctg	cgc	ttc	atc	cag	870
Leu	Asn	Val	Gln	Arg	Val	Leu	Thr	Phe	Gln	Pro	Leu	Arg	Phe	Ile	Gln	
	265					270					275					
gag	cac	gtc	ctg	atc	cct	gtc	ttt	gac	ctc	agc	ggc	ccc	agc	agt	ctg	918
Glu	His	Val	Leu	Ile	Pro	Val	Phe	Asp	Leu	Ser	Gly	Pro	Ser	Ser	Leu	
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gcc	cag	cct	gtc	cag	tac	tcc	cag	atc	agg	gtg	tct	gga	ccc	agg	gag	966
Ala	Gln	Pro	Val	Gln	Tyr	Ser	Gln	Ile	Arg	Val	Ser	Gly	Pro	Arg	Glu	
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ccc	gca	gga	gct	cca	cag	cgg	cat	agc	ctg	tcc	gag	atc	acc	tac	tta	1014
Pro	Ala	Gly	Ala	Pro	Gln	Arg	His	Ser	Leu	Ser	Glu	Ile	Thr	Tyr	Leu	
			315					320					325			

ggg	cag	cca	gac	atc	tcc	atc	ctc	cag	ccc	tcc	aac	gtg	cca	cct	ccc	1062
Gly	Gln	Pro	Asp	Ile	Ser	Ile	Leu	Gln	Pro	Ser	Asn	Val	Pro	Pro	Pro	
		330					335					340				
cag	atc	ctc	tcc	cca	ctg	tcc	tat	gcc	cca	aac	gct	gcc	cct	gag	gtc	1110
Gln	Ile	Leu	Ser	Pro	Leu	Ser	Tyr	Ala	Pro	Asn	Ala	Ala	Pro	Glu	Val	
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Gly	Pro	Pro	Ser	Tyr	Ala	Pro	Gln	Val	Thr	Pro	Glu	Ala	Gln	Phe	Pro	
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ttc	tac	gcc	cca	cag	gcc	atc	tct	aag	gtc	cag	cct	tcc	tcc	tat	gcc	1206
Phe	Tyr	Ala	Pro	Gln	Ala	Ile	Ser	Lys	Val	Gln	Pro	Ser	Ser	Tyr	Ala	
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cct	caa	gcc	act	ccg	gac	agc	tgg	cct	ccc	tcc	tat	ggg	gta	tgc	atg	1254
Pro	Gln	Ala	Thr	Pro	Asp	Ser	Trp	Pro	Pro	Ser	Tyr	Gly	Val	Cys	Met	
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gaa	ggt	tct	ggc	aaa	gac	tcc	ccc	act	ggg	aca	ctt	tct	agt	cct	aaa	1302
Glu	Gly	Ser	Gly	Lys	Asp	Ser	Pro	Thr	Gly	Thr	Leu	Ser	Ser	Pro	Lys	
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His	Leu	Arg	Pro	Lys	Gly	Gln	Leu	Gln	Lys	Glu	Pro	Pro	Ala	Gly	Ser	
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tgc	atg	tta	ggt	ggc	ctt	tct	ctg	cag	gag	gtg	acc	tcc	ttg	gct	atg	1398
Cys	Met	Leu	Gly	Gly	Leu	Ser	Leu	Gln	Glu	Val	Thr	Ser	Leu	Ala	Met	
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Glu	Glu	Ser	Gln	Glu	Ala	Lys	Ser	Leu	His	Gln	Pro	Leu	Gly	Ile	Cys	
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Thr	Asp	Arg	Thr	Ser	Asp	Pro	Asn	Val	Leu	His	Ser	Gly	Glu	Glu	Gly	
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Thr	Pro	Gln	Tyr	Leu	Lys	Gly	Gln	Leu	Pro	Leu	Leu	Ser	Ser	Val	Gln	
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atc	gag	ggc	cac	ccc	atg	tcc	ctc	cct	ttg	caa	cct	cct	tcc	ggt	cca	1590
Ile	Glu	Gly	His	Pro	Met	Ser	Leu	Pro	Leu	Gln	Pro	Pro	Ser	Gly	Pro	
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tgt	tcc	ccc	tcg	gac	caa	ggt	cca	agt	ccc	tgg	ggc	ctg	ctg	gag	tcc	1638
Cys	Ser	Pro	Ser	Asp	Gln	Gly	Pro	Ser	Pro	Trp	Gly	Leu	Leu	Glu	Ser	
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ctt	gtg	tgt	ccc	aag	gat	gaa	gcc	aag	agc	cca	gcc	cct	gag	acc	tca	1686
Leu	Val	Cys	Pro	Lys	Asp	Glu	Ala	Lys	Ser	Pro	Ala	Pro	Glu	Thr	Ser	
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gac	ctg	gag	cag	ccc	aca	gaa	ctg	gat	tct	ctt	ttc	aga	ggc	ctg	gcc	1734
Asp	Leu	Glu	Gln	Pro	Thr	Glu	Leu	Asp	Ser	Leu	Phe	Arg	Gly	Leu	Ala	
			555					560					565			
ctg	act	gtg	cag	tgg	gag	tcc	tgaggggaat	gggaaaggct	tggtgcttcc							1785

Leu Thr Val Gln Trp Glu Ser
570

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tccctgtccc taccagtggt cacatccttg gctgtcaatc ccatgcctgc ccatgccaca 1845
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<210> 2

<211> 574

<212> PRT

<213> Homo sapiens

<400> 2

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20          25          30
Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
35          40          45
Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
50          55          60
Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
65          70          75          80
Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val
85          90          95
Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg
100         105         110
Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
115         120         125
Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
130         135         140
Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
145         150         155         160
His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
165         170         175
Met His Leu Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
180         185         190
Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp
195         200         205
Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
210         215         220
Arg Thr Trp Thr Tyr Ser Phe Ser Gly Ala Phe Leu Phe Ser Met Gly
225         230         235         240
Phe Leu Val Ala Val Leu Cys Tyr Leu Ser Tyr Arg Tyr Val Thr Lys
245         250         255
Pro Pro Ala Pro Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe
260         265         270

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Gln Pro Leu Arg Phe Ile Gln Glu His Val Leu Ile Pro Val Phe Asp
 275 280 285
 Leu Ser Gly Pro Ser Ser Leu Ala Gln Pro Val Gln Tyr Ser Gln Ile
 290 295 300
 Arg Val Ser Gly Pro Arg Glu Pro Ala Gly Ala Pro Gln Arg His Ser
 305 310 315 320
 Leu Ser Glu Ile Thr Tyr Leu Gly Gln Pro Asp Ile Ser Ile Leu Gln
 325 330 335
 Pro Ser Asn Val Pro Pro Pro Gln Ile Leu Ser Pro Leu Ser Tyr Ala
 340 345 350
 Pro Asn Ala Ala Pro Glu Val Gly Pro Pro Ser Tyr Ala Pro Gln Val
 355 360 365
 Thr Pro Glu Ala Gln Phe Pro Phe Tyr Ala Pro Gln Ala Ile Ser Lys
 370 375 380
 Val Gln Pro Ser Ser Tyr Ala Pro Gln Ala Thr Pro Asp Ser Trp Pro
 385 390 395 400
 Pro Ser Tyr Gly Val Cys Met Glu Gly Ser Gly Lys Asp Ser Pro Thr
 405 410 415
 Gly Thr Leu Ser Ser Pro Lys His Leu Arg Pro Lys Gly Gln Leu Gln
 420 425 430
 Lys Glu Pro Pro Ala Gly Ser Cys Met Leu Gly Gly Leu Ser Leu Gln
 435 440 445
 Glu Val Thr Ser Leu Ala Met Glu Glu Ser Gln Glu Ala Lys Ser Leu
 450 455 460
 His Gln Pro Leu Gly Ile Cys Thr Asp Arg Thr Ser Asp Pro Asn Val
 465 470 475 480
 Leu His Ser Gly Glu Gly Thr Pro Gln Tyr Leu Lys Gly Gln Leu
 485 490 495
 Pro Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Met Ser Leu Pro
 500 505 510
 Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln Gly Pro Ser
 515 520 525
 Pro Trp Gly Leu Leu Glu Ser Leu Val Cys Pro Lys Asp Glu Ala Lys
 530 535 540
 Ser Pro Ala Pro Glu Thr Ser Asp Leu Glu Gln Pro Thr Glu Leu Asp
 545 550 555 560
 Ser Leu Phe Arg Gly Leu Ala Leu Thr Val Gln Trp Glu Ser
 565 570

<210> 3

<211> 211

<212> PRT

<213> Homo sapiens

<400> 3

Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser Ser
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 Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp
 35 40 45
 Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu
 50 55 60
 Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr
 65 70 75 80
 Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg Phe
 85 90 95
 Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys Ile
 100 105 110
 Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr Pro
 115 120 125

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Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe His
 130          135          140
Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln Met
145          150          155          160
His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro
          165          170          175
Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp Ala
          180          185          190
Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp Arg
 195          200          205
Thr Trp Thr
 210

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<210> 4

<211> 541

<212> PRT

<213> Artificial Sequence

<220>

<223> A Soluble IL-22RA-Fc Fusion Polypeptide

<400> 4

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Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro
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Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp
          35          40          45
Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu
          50          55          60
Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr
65          70          75          80
Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg Phe
          85          90          95
Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys Ile
          100          105          110
Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr Pro
          115          120          125
Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe His
          130          135          140
Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln Met
145          150          155          160
His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro
          165          170          175
Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp Ala
          180          185          190
Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp Arg
          195          200          205
Thr Trp Thr Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
          210          215          220
Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
225          230          235          240
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
          245          250          255
Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
          260          265          270
Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
          275          280          285
Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
          290          295          300
Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys

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305					310					315					320
Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu
				325					330					335	
Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu
			340					345					350		
Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys
		355				360					365				
Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys
	370					375				380					
Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu
	385				390				395						400
Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys
			405					410						415	
Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys
		420						425					430		
Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser
	435						440					445			
Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys
	450					455					460				
Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln
	465				470				475						480
Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly
			485					490						495	
Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln
		500					505					510			
Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn
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His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys			
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<210> 5

<211> 1116

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (21)...(557)

<400> 5

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Leu Met Gly Thr Leu Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu	
15 20 25	

gta cag gga gga gca gct gcg ccc atc agc tcc cac tgc agg ctt gac	149
Val Gln Gly Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp	
30 35 40	

aag tcc aac ttc cag cag ccc tat atc acc aac cgc acc ttc atg ctg	197
Lys Ser Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu	
45 50 55	

gct aag gag gct agc ttg gct gat aac aac aca gac gtt cgt ctc att	245
Ala Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile	
60 65 70 75	

ggg gag aaa ctg ttc cac gga gtc agt atg agt gag cgc tgc tat ctg	293
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Gly	Glu	Lys	Leu	Phe	His	Gly	Val	Ser	Met	Ser	Glu	Arg	Cys	Tyr	Leu		
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Met	Lys	Gln	Val	Leu	Asn	Phe	Thr	Leu	Glu	Glu	Val	Leu	Phe	Pro	Gln		
			95					100					105				
tct	gat	agg	ttc	cag	cct	tat	atg	cag	gag	gtg	gtg	ccc	ttc	ctg	gcc		389
Ser	Asp	Arg	Phe	Gln	Pro	Tyr	Met	Gln	Glu	Val	Val	Pro	Phe	Leu	Ala		
		110					115					120					
agg	ctc	agc	aac	agg	cta	agc	aca	tgt	cat	att	gaa	ggg	gat	gac	ctg		437
Arg	Leu	Ser	Asn	Arg	Leu	Ser	Thr	Cys	His	Ile	Glu	Gly	Asp	Asp	Leu		
	125						130					135					
cat	atc	cag	agg	aat	gtg	caa	aag	ctg	aag	gac	aca	gtg	aaa	aag	ctt		485
His	Ile	Gln	Arg	Asn	Val	Gln	Lys	Leu	Lys	Asp	Thr	Val	Lys	Lys	Leu		
	140					145				150					155		
gga	gag	agt	gga	gag	atc	aaa	gca	att	gga	gaa	ctg	gat	ttg	ctg	ttt		533
Gly	Glu	Ser	Gly	Glu	Ile	Lys	Ala	Ile	Gly	Glu	Leu	Asp	Leu	Leu	Phe		
				160					165					170			
atg	tct	ctg	aga	aat	gcc	tgc	att	tgaccagagc	aaagctgaaa	aatgaataac							587
Met	Ser	Leu	Arg	Asn	Ala	Cys	Ile										
			175														
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aaaggaagat	gggaagccaa	actccatcat	gatgggtgga	ttccaaatga	acccctgcgt												707
tagttacaaa	ggaaaccaat	gccacttttg	tttataagac	cagaaggtag	acttttctaag												767
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atTTTTTaaa	taattgtctt	tttccataaa	aaagattact	ttccattcct	ttaggggaaa												887
aaacccctaa	atagcttcat	gtttccataa	tcagtacttt	atattttataa	atgtattttat												947
tattattata	agactgcatt	ttattttatat	catttttatta	atatggattt	atttatagaa												1007
acatcattcg	atattgctac	ttgagtgtaa	ggctaataatt	gatattttatg	acaataatta												1067
tagagctata	acatgtttat	ttgacctcaa	taaacacttg	gatataccta													1116

<210> 6
 <211> 179
 <212> PRT
 <213> Homo sapiens

<400> 6
 Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe Leu Met Gly Thr Leu
 1 5 10 15
 Ala Thr Ser Cys Leu Leu Leu Ala Leu Leu Val Gln Gly Gly Ala
 20 25 30
 Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln
 35 40 45
 Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
 50 55 60
 Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
 65 70 75 80
 His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu
 85 90 95
 Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln
 100 105 110
 Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg
 115 120 125
 Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn
 130 135 140
 Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu


```

145             150             155             160
Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
                165             170             175
Ala Cys Ile

```

```
<210> 7
<211> 926
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (45) ... (575)
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<221> variation
<222> (188)...(188)
<223> Nucleotide may be C or G at position 188
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<400> 7
ctttgaattc ctagctcctg tggctctcag atttcaggcc taag atg aaa gcc tct      56
                               Met Lys Ala Ser
                               1
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agt ctt gcc ttc agc ctt ctc tct gct gcg ttt tat ctc cta tgg act 104
 Ser Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr Leu Leu Trp Thr
 5 10 15 20

cct tcc act gga ctg aag aca ctc aat ttg gga agc tgt gtg atc gcc 152
Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser Cys Val Ile Ala
25 30 35

aca aac ctt cag gaa ata cga aat gga ttt tct gas ata cgg ggc agt 200
Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Xaa Ile Arg Gly Ser
40 45 50

gtg caa gcc aaa gat gga aac att gac atc aga atc tta agg agg act 248
Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile Leu Arg Arg Thr
55 60 65

gag tct ttg caa gac aca aag cct gcg aat cga tgc tgc ctc ctg cgc 296
Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys Cys Leu Leu Arg
70 75 80

cat	ttg	cta	aga	ctc	tat	ctg	gac	agg	gta	ttt	aaa	aac	tac	cag	acc	344
His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	Lys	Asn	Tyr	Gln	Thr	
85					90					95					100	

cct gac cat tat act ctc cgg aag atc agc agc ctc gcc aat tcc ttt 392
Pro Asp His Tyr Thr Leu Arg Lys Ile Ser Ser Leu Ala Asn Ser Phe
105 110 115

ctt acc atc aag aag gac ctc cgg ctc tgt cat gcc cac atg aca tgc 440
Leu Thr Ile Lys Lys Asp Leu Arg Leu Cys His Ala His Met Thr Cys
120 125 130

cat tgt ggg gag gaa gca atg aag aaa tac agc cag att ctg agt cac 488
His Cys Gly Glu Glu Ala Met Lys Lys Tyr Ser Gln Ile Leu Ser His
135 140 145

ttt gaa aag ctg gaa cct cag gca gca gtt gtg aag gct ttg ggg gaa 536

Phe Glu Lys Leu Glu Pro Gln Ala Ala Val Val Lys Ala Leu Gly Glu
 150 155 160

cta gac att ctt ctg caa tgg atg gag gag aca gaa tag gaggaagtg 585
 Leu Asp Ile Leu Leu Gln Trp Met Glu Glu Thr Glu *
 165 170 175

atgctgctgc taagaatatt cgaggtcaag agctccagtc ttcaataacct gcagaggagg 645
 catgacccca aaccaccatc tctttactgt actagtcttg tgctgggtcac agtgtatctt 705
 atttatgcat tacttgcttc cttgcatgat tgtctttatg catccccaat cttaattgag 765
 accatacttg tataagattt ttgtaatatc tttctgctat tggatatatt tattagttaa 825
 tatattttatt tatttttttgc tattaatgta ttttaattttt tacttggggca tgaaacttta 885
 aaaaaaattc acaagattat atttataacc tgactagagc a 926

<210> 8
 <211> 176
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (48)...(48)
 <223> Amino acid at position 48 can be a D (Asp) or E (Glu)

<221> VARIANT
 <222> 48
 <223> Xaa = Any Amino Acid

<400> 8
 Met Lys Ala Ser Ser Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr
 1 5 10 15
 Leu Leu Trp Thr Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser
 20 25 30
 Cys Val Ile Ala Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Xaa
 35 40 45
 Ile Arg Gly Ser Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile
 50 55 60
 Leu Arg Arg Thr Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys
 65 70 75 80
 Cys Leu Leu Arg His Leu Leu Arg Leu Tyr Leu Asp Arg Val Phe Lys
 85 90 95
 Asn Tyr Gln Thr Pro Asp His Tyr Thr Leu Arg Lys Ile Ser Ser Leu
 100 105 110
 Ala Asn Ser Phe Leu Thr Ile Lys Lys Asp Leu Arg Leu Cys His Ala
 115 120 125
 His Met Thr Cys His Cys Gly Glu Glu Ala Met Lys Lys Tyr Ser Gln
 130 135 140
 Ile Leu Ser His Phe Glu Lys Leu Glu Pro Gln Ala Ala Val Val Lys
 145 150 155 160
 Ala Leu Gly Glu Leu Asp Ile Leu Leu Gln Trp Met Glu Glu Thr Glu
 165 170 175

<210> 9
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide Linker

<400> 9

Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

<210> 10

<211> 1050

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (5)...(589)

<400> 10

aaca ggc tct cct ctc act tat caa ctt ttg aca ctt gtg cga tcg gtg 49
 Gly Ser Pro Leu Thr Tyr Gln Leu Leu Thr Leu Val Arg Ser Val
 1 5 10 15

atg gct gtc ctg cag aaa tct atg agt ttt tcc ctt atg ggg act ttg 97
 Met Ala Val Leu Gln Lys Ser Met Ser Phe Ser Leu Met Gly Thr Leu
 20 25 30

gcc gcc agc tgc ctg ctt ctc att gcc ctg tgg gcc cag gag gca aat 145
 Ala Ala Ser Cys Leu Leu Leu Ile Ala Leu Trp Ala Gln Glu Ala Asn
 35 40 45

gcg ctg ccc atc aac acc cgg tgc aag ctt gag gtg tcc aac ttc cag 193
 Ala Leu Pro Ile Asn Thr Arg Cys Lys Leu Glu Val Ser Asn Phe Gln
 50 55 60

cag ccg tac atc gtc aac cgc acc ttt atg ctg gcc aag gag gcc agc 241
 Gln Pro Tyr Ile Val Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
 65 70 75

ctt gca gat aac aac aca gac gtc cgg ctg atc ggg gag aaa ctg ttc 289
 Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
 80 85 90 95

cga gga gtc agt gct aag gat cag tgc tac ctg atg aag cag gtg ctc 337
 Arg Gly Val Ser Ala Lys Asp Gln Cys Tyr Leu Met Lys Gln Val Leu
 100 105 110

aac ttc acc ctg gaa gac att ctg ctc ccc cag tca gac agg ttc cgg 385
 Asn Phe Thr Leu Glu Asp Ile Leu Leu Pro Gln Ser Asp Arg Phe Arg
 115 120 125

ccc tac atg cag gag gtg gtg cct ttc ctg acc aaa ctc agc aat cag 433
 Pro Tyr Met Gln Glu Val Val Pro Phe Leu Thr Lys Leu Ser Asn Gln
 130 135 140

ctc agc tcc tgt cac atc agt ggt gac gac cag aac atc cag aag aat 481
 Leu Ser Ser Cys His Ile Ser Gly Asp Asp Gln Asn Ile Gln Lys Asn
 145 150 155

gtc aga agg ctg aag gag aca gtg aaa aag ctt gga gag agc gga gag 529
 Val Arg Arg Leu Lys Glu Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
 160 165 170 175

atc aaa gcg atc ggg gaa ctg gac ctg ctg ttt atg tct ctg aga aat 577
 Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
 180 185 190

gct tgc gtc tga gcgagaagaa gctagaaaac gaagaactgc tccttcctgc 629
Ala Cys Val *

cttctaataaa gaacaataag atccctgaat ggactttttt actaaaggaa agtgagaagc 689
taacgtccac catcattaga agatttcaca tgaaacctgg ctcagttgaa agagaaaata 749
gtgtcaagtt gtccatgaga ccagaggttag acttgataac cacaaagatt cattgacaat 809
atattattgt cattgataat gcaacagaaa aagtatgtac tttaaaaaat tgtttgaaag 869
gaggttacct ctcattcctc tagaagaaaa gcctatgtaa cttcatttcc ataaccaata 929
ctttatatat gtaagtttat ttattataag tatacatttt atttatgtca gtttattaat 989
atggatttat ttatagaaaa attatctgat gttgatattt gagtataaag caaataatat 1049
t 1050

<210> 11
<211> 194
<212> PRT
<213> Mus musculus

<400> 11
Gly Ser Pro Leu Thr Tyr Gln Leu Leu Thr Leu Val Arg Ser Val Met
1 5 10 15
Ala Val Leu Gln Lys Ser Met Ser Phe Ser Leu Met Gly Thr Leu Ala
20 25 30
Ala Ser Cys Leu Leu Leu Ile Ala Leu Trp Ala Gln Glu Ala Asn Ala
35 40 45
Leu Pro Ile Asn Thr Arg Cys Lys Leu Glu Val Ser Asn Phe Gln Gln
50 55 60
Pro Tyr Ile Val Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu
65 70 75 80
Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe Arg
85 90 95
Gly Val Ser Ala Lys Asp Gln Cys Tyr Leu Met Lys Gln Val Leu Asn
100 105 110
Phe Thr Leu Glu Asp Ile Leu Leu Pro Gln Ser Asp Arg Phe Arg Pro
115 120 125
Tyr Met Gln Glu Val Val Pro Phe Leu Thr Lys Leu Ser Asn Gln Leu
130 135 140
Ser Ser Cys His Ile Ser Gly Asp Asp Gln Asn Ile Gln Lys Asn Val
145 150 155 160
Arg Arg Leu Lys Glu Thr Val Lys Lys Leu Gly Glu Ser Gly Glu Ile
165 170 175
Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn Ala
180 185 190
Cys Val

<210> 12
<211> 2149
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(693)

<400> 12
atg atg cct aaa cat tgc ttt cta ggc ttc ctc atc agt ttc ttc ctt 48
Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
1 5 10 15

act ggt gta gca gga act cag tca acg cat gag tct ctg aag cct cag	96
Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln	
20 25 30	
agg gta caa ttt cag tcc cga aat ttt cac aac att ttg caa tgg cag	144
Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln	
35 40 45	
cct ggg agg gca ctt act ggc aac agc agt gtc tat ttt gtg cag tac	192
Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr	
50 55 60	
aaa ata tat gga cag aga caa tgg aaa aat aaa gaa gac tgt tgg ggt	240
Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly	
65 70 75 80	
act caa gaa ctc tct tgt gac ctt acc agt gaa acc tca gac ata cag	288
Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln	
85 90 95	
gaa cct tat tac ggg agg gtg agg gcg gcc tcg gct ggg agc tac tca	336
Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser	
100 105 110	
gaa tgg agc atg acg ccg cgg ttc act ccc tgg tgg gaa aca aaa ata	384
Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile	
115 120 125	
gat cct cca gtc atg aat ata acc caa gtc aat ggc tct ttg ttg gta	432
Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val	
130 135 140	
att ctc cat gct cca aat tta cca tat aga tac caa aag gaa aaa aat	480
Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn	
145 150 155 160	
gta tct ata gaa gat tac tat gaa cta cta tac cga gtt ttt ata att	528
Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile	
165 170 175	
aac aat tca cta gaa aag gag caa aag gtt tat gaa ggg gct cac aga	576
Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg	
180 185 190	
gcg gtt gaa att gaa gct cta aca cca cac tcc agc tac tgt gta gtg	624
Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val	
195 200 205	
gct gaa ata tat cag ccc atg tta gac aga aga agt cag aga agt gaa	672
Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu	
210 215 220	
gag aga tgt gtg gaa att cca tgacttggtg aatttgcat tcagcaatgt	723
Glu Arg Cys Val Glu Ile Pro	
225 230	
ggaaattcta aagctccctg agaacaggat gactcgtgtt tgaaggatct tatttaaaat	783
tggttttgta ttttcttaaa gcaatattca ctgttacacc ttggggactt cttgtttat	843
ccattctttt atcctttata tttcatttta aactatatatt gaacgacatt cccccgaaa	903
aattgaaatg taaagatgag gcagagaata aagtgttcta tgaaattcag aactttatatt	963
ctgaatgtaa catccctaata aacaaccttc attctttctaa tacagcaaaa taaaaattta	1023
acaaccaagg aatagtattt aagaaaatgt tgaaataatt tttttaaaat agcattacag	1083

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actgaggcgg tctgaagca atgggttttc actctcttat tgagccaatt aaattgacat 1143
tgctttgaca atttaaaact tctataaagg tgaatatatt tcatacattt ctattttata 1203
tgaatatact ttttatatat ttattattat taaatatatt tacttaatga atcaaaattt 1263
tgttttaaag tctactttat gtaaataaga acagggtttg gggaaaaaaa tcttatgatt 1323
tctggattga tatctgaatt aaaactatca acaacaagga agtctactct gtacaattgt 1383
ccctcattta aaagatatat taagcttttc ttttctggtt gtttttggtt tgtttagttt 1443
ttaatcctgt cttagaagaa cttatcttta ttctcaaaat taaatgtaat ttttttagtg 1503
acaaagaaga aaggaaacct cattactcaa tccttctggc caagagtgtc ttgcttggtg 1563
cgccttcctc atctctatat aggaggatcc catgaatgat ggtttattgg gaactgctgg 1623
ggtcgacccc atacagagaa ctcagcttga agctggaagc acacagtggg tagcaggaga 1683
aggaccggtg ttggtaggtg cctacagaga ctatagagct agacaaagcc ctccaaactg 1743
gcccctcctg ctcactgcct ctcctgagta gaaatctggt gacctaaagg tcagtgcggt 1803
caacagaaaag ctgccttctt cacttgaggc taagtcttca tatatgttta aggttgcctt 1863
tctagtgagg agatacatat cagagaacat ttgtacaatt ccccatgaaa attgctccaa 1923
agttgataac aatatagtcg gtgcttctag ttatatgcaa gtactcagtg ataaatggat 1983
taaaaaatat tcagaaatgt attggggggg ggaggagaat aagaggcaga gcaagagcta 2043
gagaattggt ttccttgctt cctgtatgc tcagaaaaca ttgatttgag catagacgca 2103
gagactgaaa aaaaaaaaaa gctcgcgcgg cgcgcatac cttggt 2149

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<210> 13
<211> 231
<212> PRT
<213> Homo sapiens

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<400> 13
Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
1 5 10 15
Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
20 25 30
Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
35 40 45
Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
50 55 60
Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
65 70 75 80
Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
85 90 95
Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
100 105 110
Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
115 120 125
Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
130 135 140
Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
145 150 155 160
Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
165 170 175
Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
180 185 190
Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
195 200 205
Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
210 215 220
Glu Arg Cys Val Glu Ile Pro
225 230

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<210> 14
<211> 699
<212> DNA
<213> Artificial Sequence

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<220>

<223> C-Terminal Fc4 tag

<400> 14

gagcccagat	cttcagacaa	aactcacaca	tgcccaccgt	gcccagcacc	tgaagccgag	60
ggggcaccgt	cagtcttcct	cttcccccca	aaacccaagg	acaccctcat	gatctcccgg	120
acccttgagg	tcacatgcgt	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	180
aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaga	caaagccgcg	ggaggagcag	240
tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgcaccagga	ctggctgaat	300
ggcaaggagt	acaagtgcaa	ggtctccaac	aaagccctcc	catcctccat	cgagaaaacc	360
atctccaaag	ccaaagggca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatcccgg	420
gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatcccagc	480
gacatcgccg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	540
cccgtgctgg	actccgacgg	ctccttcttc	ctctacagca	agctcaccgt	ggacaagagc	600
aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	660
tacacgcaga	agagcctctc	cctgtctccg	ggtaaataa			699

<210> 15

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Glu-Glu (CEE) Peptide Tag

<400> 15

Glu	Tyr	Met	Pro	Met	Glu
1				5	

<210> 16

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Glu-Glu (CEE) Peptide Tag with spacer

<400> 16

Gly	Ser	Gly	Gly	Glu	Tyr	Met	Pro	Met	Glu
1				5					10

<210> 17

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC39289

<400> 17

tccgaggagt caatgctaag

20

<210> 18

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide Primer ZC39290

<400> 18
 tccaagcttt ttcactgtct 20

 <210> 19
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Primer ZC39776

 <400> 19
 gggcccgcta gcacct 16

 <210> 20
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Primer ZC39777

 <400> 20
 gggatgatccg ctggca 16

 <210> 21
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> IL-20 FAM/TAMRA labeled TaqMan probe ZC38752

 <400> 21
 ccagccactt tctctctccg tatttcttat attcca 36

 <210> 22
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> forward primer, ZC42459

 <400> 22
 tggccaggct cagcaa 16

 <210> 23
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> reverse primer, ZC42458

 <400> 23
 gcacattcct ctggatatgc a 21

 <210> 24
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-22 TaqMan probe, ZC42460

 <400> 24
 aggctaagca catgtcatat tgaaggatg g 31

 <210> 25
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> forward primer, ZC40541

 <400> 25
 tcgccaattc ctttcttacc a 21

 <210> 26
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> reverse primer, ZC40542

 <400> 26
 cccacaatgg catgtcatgt 20

 <210> 27
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> IL-20 TaqMan® probe ZC40544

 <400> 27
 agaaggacct ccggtctgt catgc 25

 <210> 28
 <211> 57
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer ZC45,593

 <400> 28
 caggaaatcc atgccgagtt gagacgcttc cgtagacacg cccctgagga ccctcg 57

 <210> 29
 <211> 63
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer ZC45,592

 <400> 29
 tctgggctca ccgcttccag acccgcttcc agaccgctt cctgtccggt ctggcagtgt 60
 ctt 63

<210> 30
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC45,591

<400> 30
 gaccggacag gaagcggggtc tggaagcggg tctggaagcg gtgagcccag aggccccaca 60
 atc 63

<210> 31
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC45,594

<400> 31
 agagctgttt taaggcgcgc ctctagatta tttttattta cccggagtcc gggagaa 57

<210> 32
 <211> 531
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)...(531)

<400> 32
 atg aaa ggc ttt ggt ctt gcc ttt gga ctg ttc tcc gct gtg ggt ttt 48
 Met Lys Gly Phe Gly Leu Ala Phe Gly Leu Phe Ser Ala Val Gly Phe
 1 5 10 15
 ctt ctc tgg act cct tta act ggg ctc aag acc ctc cat ttg gga agc 96
 Leu Leu Trp Thr Pro Leu Thr Gly Leu Lys Thr Leu His Leu Gly Ser
 20 25 30
 tgt gtg att act gca aac cta cag gca ata caa aag gaa ttt tct gag 144
 Cys Val Ile Thr Ala Asn Leu Gln Ala Ile Gln Lys Glu Phe Ser Glu
 35 40 45
 att cgg gat agt gtg caa gct gaa gat aca aat att gac atc aga att 192
 Ile Arg Asp Ser Val Gln Ala Glu Asp Thr Asn Ile Asp Ile Arg Ile
 50 55 60
 tta agg acg act gag tct ttg aaa gac ata aag tct ttg gat agg tgc 240
 Leu Arg Thr Thr Glu Ser Leu Lys Asp Ile Lys Ser Leu Asp Arg Cys
 65 70 75 80
 tgc ttc ctt cgt cat cta gtg aga ttc tat ctg gac agg gta ttc aaa 288
 Cys Phe Leu Arg His Leu Val Arg Phe Tyr Leu Asp Arg Val Phe Lys
 85 90 95
 gtc tac cag acc cct gac cac cat acc ctg aga aag atc agc agc ctc 336
 Val Tyr Gln Thr Pro Asp His His Thr Leu Arg Lys Ile Ser Ser Leu
 100 105 110

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gcc aac tcc ttt ctt atc atc aag aag gac ctc tca gtc tgt cat tct 384
Ala Asn Ser Phe Leu Ile Ile Lys Lys Asp Leu Ser Val Cys His Ser
      115                      120                      125

cac atg gca tgt cat tgt ggg gaa gaa gca atg gag aaa tac aac caa 432
His Met Ala Cys His Cys Gly Glu Glu Ala Met Glu Lys Tyr Asn Gln
      130                      135                      140

att ctg agt cac ttc ata gag ttg gaa ctt cag gca gcg gtg gta aag 480
Ile Leu Ser His Phe Ile Glu Leu Glu Leu Gln Ala Ala Val Val Lys
      145                      150                      155                      160

gct ttg gga gaa cta ggc att ctt ctg aga tgg atg gag gag atg cta 528
Ala Leu Gly Glu Leu Gly Ile Leu Leu Arg Trp Met Glu Glu Met Leu
      165                      170                      175

tag 531
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<210> 33
<211> 176
<212> PRT
<213> Mus musculus
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<400> 33
Met Lys Gly Phe Gly Leu Ala Phe Gly Leu Phe Ser Ala Val Gly Phe
 1      5      10      15
Leu Leu Trp Thr Pro Leu Thr Gly Leu Lys Thr Leu His Leu Gly Ser
      20      25      30
Cys Val Ile Thr Ala Asn Leu Gln Ala Ile Gln Lys Glu Phe Ser Glu
      35      40      45
Ile Arg Asp Ser Val Gln Ala Glu Asp Thr Asn Ile Asp Ile Arg Ile
      50      55      60
Leu Arg Thr Thr Glu Ser Leu Lys Asp Ile Lys Ser Leu Asp Arg Cys
      65      70      75      80
Cys Phe Leu Arg His Leu Val Arg Phe Tyr Leu Asp Arg Val Phe Lys
      85      90      95
Val Tyr Gln Thr Pro Asp His His Thr Leu Arg Lys Ile Ser Ser Leu
      100      105      110
Ala Asn Ser Phe Leu Ile Ile Lys Lys Asp Leu Ser Val Cys His Ser
      115      120      125
His Met Ala Cys His Cys Gly Glu Glu Ala Met Glu Lys Tyr Asn Gln
      130      135      140
Ile Leu Ser His Phe Ile Glu Leu Glu Leu Gln Ala Ala Val Val Lys
      145      150      155      160
Ala Leu Gly Glu Leu Gly Ile Leu Leu Arg Trp Met Glu Glu Met Leu
      165      170      175
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<210> 34
<211> 21
<212> DNA
<213> Artificial Sequence
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<220>
<223> Oligonucleotide primer ZC22901
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<400> 34
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<210> 35
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer ZC45039

 <400> 35
 attaggcttg ggaggggaatg g 21

 <210> 36
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer ZC38573

 <400> 36
 tggcgatgcc tgcttgccga ata 23

 <210> 37
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer ZC25223

 <400> 37
 gtcttcctca catctgttat cg 22

 <210> 38
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer ZC40128

 <400> 38
 ggcttgaact ttgagaaagg cagt 24

 <210> 39
 <211> 1473
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> IL-22RA Extracellular domain with tPA leader and
 fused to murine gamma 2a heavy chain Fc region
 (mG2a)

 <221> CDS
 <222> (1)...(1473)

 <400> 39
 atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg ctg ctg tgt ggc 48
 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15

gcc gtc ttc gtt tcg ctc agc cag gaa atc cat gcc gag ttg aga cgc	96
Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg	
20 25 30	
ttc cgt aga cac gcc cct gag gac ccc tcg gat ctg ctc cag cac gtg	144
Phe Arg Arg His Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val	
35 40 45	
aaa ttc cag tcc agc aac ttt gaa aac atc ctg acg tgg gac agc ggg	192
Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly	
50 55 60	
cca gag ggc acc cca gac acg gtc tac agc atc gag tat aag acg tac	240
Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr	
65 70 75 80	
gga gag agg gac tgg gtg gca aag aag ggc tgt cag cgg atc acc cgg	288
Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg	
85 90 95	
aag tcc tgc aac ctg acg gtg gag acg ggc aac ctc acg gag ctc tac	336
Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr	
100 105 110	
tat gcc agg gtc acc gct gtc agt gcg gga ggc cgg tca gcc acc aag	384
Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys	
115 120 125	
atg act gac agg ttc agc tct ctg cag cac act acc ctc aag cca cct	432
Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro	
130 135 140	
gat gtg acc tgt atc tcc aaa gtg aga tcg att cag atg att gtt cat	480
Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His	
145 150 155 160	
cct acc ccc acg cca atc cgt gca ggc gat ggc cac cgg cta acc ctg	528
Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu	
165 170 175	
gaa gac atc ttc cat gac ctg ttc tac cac tta gag ctc cag gtc aac	576
Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn	
180 185 190	
cgc acc tac caa atg cac ctt gga ggg aag cag aga gaa tat gag ttc	624
Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe	
195 200 205	
ttc ggc ctg acc cct gac aca gag ttc ctt ggc acc atc atg att tgc	672
Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys	
210 215 220	
gtt ccc acc tgg gcc aag gag agt gcc ccc tac atg tgc cga gtg aag	720
Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys	
225 230 235 240	
aca ctg cca gac cgg aca gga agc ggg tct gga agc ggg tct gga agc	768
Thr Leu Pro Asp Arg Thr Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser	
245 250 255	
ggt gag ccc aga ggc ccc aca atc aag ccc tgt cct cca tgc aaa tgc	816
Gly Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys	

260										265					270					
cca	gca	cct	aac	ctc	ttg	ggt	gga	cca	tcc	gtc	ttc	atc	ttc	cct	cca	864				
Pro	Ala	Pro	Asn	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro					
		275					280					285								
aag	atc	aag	gat	gta	ctc	atg	atc	tcc	ctg	agc	ccc	ata	gtc	aca	tgt	912				
Lys	Ile	Lys	Asp	Val	Leu	Met	Ile	Ser	Leu	Ser	Pro	Ile	Val	Thr	Cys					
	290					295					300									
gtg	gtg	gtg	gat	gtg	agc	gag	gat	gac	cca	gat	gtc	cag	atc	agc	tgg	960				
Val	Val	Val	Asp	Val	Ser	Glu	Asp	Asp	Pro	Asp	Val	Gln	Ile	Ser	Trp					
305					310					315					320					
ttt	gtg	aac	aac	gtg	gaa	gta	cac	aca	gct	cag	aca	caa	acc	cat	aga	1008				
Phe	Val	Asn	Asn	Val	Glu	Val	His	Thr	Ala	Gln	Thr	Gln	Thr	His	Arg					
				325					330					335						
gag	gat	tac	aac	agt	act	ctc	cgg	gtg	gtc	agt	gcc	ctc	ccc	atc	cag	1056				
Glu	Asp	Tyr	Asn	Ser	Thr	Leu	Arg	Val	Val	Ser	Ala	Leu	Pro	Ile	Gln					
			340					345					350							
cac	cag	gac	tgg	atg	agt	ggc	aag	gag	ttc	aaa	tgc	aag	gtc	aac	aac	1104				
His	Gln	Asp	Trp	Met	Ser	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn					
		355					360					365								
aaa	gac	ctc	cca	gcg	ccc	atc	gag	aga	acc	atc	tca	aaa	ccc	aaa	ggg	1152				
Lys	Asp	Leu	Pro	Ala	Pro	Ile	Glu	Arg	Thr	Ile	Ser	Lys	Pro	Lys	Gly					
	370					375					380									
tca	gta	aga	gct	cca	cag	gta	tat	gtc	ttg	cct	cca	cca	gaa	gaa	gag	1200				
Ser	Val	Arg	Ala	Pro	Gln	Val	Tyr	Val	Leu	Pro	Pro	Pro	Glu	Glu	Glu					
385					390					395					400					
atg	act	aag	aaa	cag	gtc	act	ctg	acc	tgc	atg	gtc	aca	gac	ttc	atg	1248				
Met	Thr	Lys	Lys	Gln	Val	Thr	Leu	Thr	Cys	Met	Val	Thr	Asp	Phe	Met					
				405					410					415						
cct	gaa	gac	att	tac	gtg	gag	tgg	acc	aac	aac	ggg	aaa	aca	gag	cta	1296				
Pro	Glu	Asp	Ile	Tyr	Val	Glu	Trp	Thr	Asn	Asn	Gly	Lys	Thr	Glu	Leu					
			420					425					430							
aac	tac	aag	aac	act	gaa	cca	gtc	ctg	gac	tct	gat	ggg	tct	tac	ttc	1344				
Asn	Tyr	Lys	Asn	Thr	Glu	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe					
		435					440					445								
atg	tac	agc	aag	ctg	aga	gtg	gaa	aag	aag	aac	tgg	gtg	gaa	aga	aat	1392				
Met	Tyr	Ser	Lys	Leu	Arg	Val	Glu	Lys	Lys	Asn	Trp	Val	Glu	Arg	Asn					
	450					455					460									
agc	tac	tcc	tgt	tca	gtg	gtc	cac	gag	ggg	ctg	cac	aat	cac	cac	acg	1440				
Ser	Tyr	Ser	Cys	Ser	Val	Val	His	Glu	Gly	Leu	His	Asn	His	His	Thr					
465					470				475						480					
act	aag	agc	ttc	tcc	cgg	act	ccg	ggg	aaa	taa						1473				
Thr	Lys	Ser	Phe	Ser	Arg	Thr	Pro	Gly	Lys	*										
				485					490											

<210> 40
 <211> 490
 <212> PRT

<213> Artificial Sequence

<220>

<223> IL-22RA Extracellular domain with tPA leader and
fused to murine gamma 2a heavy chain Fc region
(mG2a)

<400> 40

Met	Asp	Ala	Met	Lys	Arg	Gly	Leu	Cys	Cys	Val	Leu	Leu	Leu	Cys	Gly
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Ala	Val	Phe	Val	Ser	Leu	Ser	Gln	Glu	Ile	His	Ala	Glu	Leu	Arg	Arg
			20					25					30		
Phe	Arg	Arg	His	Ala	Pro	Glu	Asp	Pro	Ser	Asp	Leu	Leu	Gln	His	Val
		35					40					45			
Lys	Phe	Gln	Ser	Ser	Asn	Phe	Glu	Asn	Ile	Leu	Thr	Trp	Asp	Ser	Gly
	50					55					60				
Pro	Glu	Gly	Thr	Pro	Asp	Thr	Val	Tyr	Ser	Ile	Glu	Tyr	Lys	Thr	Tyr
65					70					75					80
Gly	Glu	Arg	Asp	Trp	Val	Ala	Lys	Lys	Gly	Cys	Gln	Arg	Ile	Thr	Arg
				85					90					95	
Lys	Ser	Cys	Asn	Leu	Thr	Val	Glu	Thr	Gly	Asn	Leu	Thr	Glu	Leu	Tyr
			100					105					110		
Tyr	Ala	Arg	Val	Thr	Ala	Val	Ser	Ala	Gly	Gly	Arg	Ser	Ala	Thr	Lys
		115					120					125			
Met	Thr	Asp	Arg	Phe	Ser	Ser	Leu	Gln	His	Thr	Thr	Leu	Lys	Pro	Pro
	130					135					140				
Asp	Val	Thr	Cys	Ile	Ser	Lys	Val	Arg	Ser	Ile	Gln	Met	Ile	Val	His
145					150					155					160
Pro	Thr	Pro	Thr	Pro	Ile	Arg	Ala	Gly	Asp	Gly	His	Arg	Leu	Thr	Leu
				165					170					175	
Glu	Asp	Ile	Phe	His	Asp	Leu	Phe	Tyr	His	Leu	Glu	Leu	Gln	Val	Asn
			180					185					190		
Arg	Thr	Tyr	Gln	Met	His	Leu	Gly	Gly	Lys	Gln	Arg	Glu	Tyr	Glu	Phe
		195					200					205			
Phe	Gly	Leu	Thr	Pro	Asp	Thr	Glu	Phe	Leu	Gly	Thr	Ile	Met	Ile	Cys
	210					215					220				
Val	Pro	Thr	Trp	Ala	Lys	Glu	Ser	Ala	Pro	Tyr	Met	Cys	Arg	Val	Lys
225					230					235					240
Thr	Leu	Pro	Asp	Arg	Thr	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser
				245					250					255	
Gly	Glu	Pro	Arg	Gly	Pro	Thr	Ile	Lys	Pro	Cys	Pro	Pro	Cys	Lys	Cys
			260					265					270		
Pro	Ala	Pro	Asn	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro
		275					280					285			
Lys	Ile	Lys	Asp	Val	Leu	Met	Ile	Ser	Leu	Ser	Pro	Ile	Val	Thr	Cys
	290					295					300				
Val	Val	Val	Asp	Val	Ser	Glu	Asp	Asp	Pro	Asp	Val	Gln	Ile	Ser	Trp
305					310					315					320
Phe	Val	Asn	Asn	Val	Glu	Val	His	Thr	Ala	Gln	Thr	Gln	Thr	His	Arg
				325					330					335	
Glu	Asp	Tyr	Asn	Ser	Thr	Leu	Arg	Val	Val	Ser	Ala	Leu	Pro	Ile	Gln
			340					345					350		
His	Gln	Asp	Trp	Met	Ser	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn
		355					360					365			
Lys	Asp	Leu	Pro	Ala	Pro	Ile	Glu	Arg	Thr	Ile	Ser	Lys	Pro	Lys	Gly
	370					375					380				
Ser	Val	Arg	Ala	Pro	Gln	Val	Tyr	Val	Leu	Pro	Pro	Pro	Glu	Glu	Glu
385					390					395					400
Met	Thr	Lys	Lys	Gln	Val	Thr	Leu	Thr	Cys	Met	Val	Thr	Asp	Phe	Met
				405					410					415	
Pro	Glu	Asp	Ile	Tyr	Val	Glu	Trp	Thr	Asn	Asn	Gly	Lys	Thr	Glu	Leu
			420					425					430		

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Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe
      435                      440          445
Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn
      450                      455          460
Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr
465                      470          475          480
Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
      485                      490

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<210> 41
<211> 1834
<212> DNA
<213> Mus musculus

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<220>
<221> CDS
<222> (43)...(1788)

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ttggtccaga gccgaggccc gaagggggccc tggaggggacc ca atg aag aca cta      54
                                         Met Lys Thr Leu
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ctg acc atc ctg acg gtg gga tcc ctg gcc gct cac acc act gtg gac      102
Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His Thr Thr Val Asp
 5                      10                      15                      20

aca tcc ggt ctc ctt caa cac gtg aaa ttc cag tcc agc aac ttt gag      150
Thr Ser Gly Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu
                      25                      30                      35

aac atc ttg acg tgg gat ggt ggg ccc gct agc acc tct gac acc gtc      198
Asn Ile Leu Thr Trp Asp Gly Gly Pro Ala Ser Thr Ser Asp Thr Val
                      40                      45                      50

tac agt gtg gaa tat aag aaa tac gga gag aga aag tgg ctg gcc aag      246
Tyr Ser Val Glu Tyr Lys Lys Tyr Gly Glu Arg Lys Trp Leu Ala Lys
                      55                      60                      65

gcg ggc tgc cag cgg atc acc cag aag ttc tgc aac ctg act atg gag      294
Ala Gly Cys Gln Arg Ile Thr Gln Lys Phe Cys Asn Leu Thr Met Glu
 70                      75                      80

acc cgc aac cac act gag ttt tac tac gcc aag gtc acg gca gtc agc      342
Thr Arg Asn His Thr Glu Phe Tyr Tyr Ala Lys Val Thr Ala Val Ser
 85                      90                      95                      100

gca gga ggc cca cca gtc aca aag atg act gat cgt ttc agc tcg ctg      390
Ala Gly Gly Pro Pro Val Thr Lys Met Thr Asp Arg Phe Ser Ser Leu
                      105                      110                      115

cag cac act acc atc aaa ccg cct gat gtg acc tgt atc ccc aaa gtg      438
Gln His Thr Thr Ile Lys Pro Pro Asp Val Thr Cys Ile Pro Lys Val
                      120                      125                      130

agg tcc att cag atg ctg gtc cac ccc aca ctc aca ccg gtc ctc tcg      486
Arg Ser Ile Gln Met Leu Val His Pro Thr Leu Thr Pro Val Leu Ser
                      135                      140                      145

gaa gat ggc cac cag cta acc ctg gag gag att ttc cat gac ctg ttc      534
Glu Asp Gly His Gln Leu Thr Leu Glu Glu Ile Phe His Asp Leu Phe

```


150	155	160	
tac cgc tta gag ctc cac gtc aac cac acc tac cag atg cac ctt gaa			582
Tyr Arg Leu Glu Leu His Val Asn His Thr Tyr Gln Met His Leu Glu			
165	170	175	180
ggc aaa cag aga gaa tac gag ttc ctt ggc ctg act ccc gac aca gag			630
Gly Lys Gln Arg Glu Tyr Glu Phe Leu Gly Leu Thr Pro Asp Thr Glu			
	185	190	195
ttc ctc ggc tcc atc aca att ttg act ccg ata ttg tcc aag gaa agt			678
Phe Leu Gly Ser Ile Thr Ile Leu Thr Pro Ile Leu Ser Lys Glu Ser			
	200	205	210
gcc ccc tac gtg tgc cga gtg aag acg ctg ccc gat cgg acg tgg gcc			726
Ala Pro Tyr Val Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Ala			
	215	220	225
tac tcc ttc tcg ggc gcc gtg ctc ttt tcc atg ggt ttc ctc gtc ggc			774
Tyr Ser Phe Ser Gly Ala Val Leu Phe Ser Met Gly Phe Leu Val Gly			
	230	235	240
ttg ctc tgt tat ctg ggc tac aaa tac atc acc aag cca cct gta cct			822
Leu Leu Cys Tyr Leu Gly Tyr Lys Tyr Ile Thr Lys Pro Pro Val Pro			
	245	250	255
cct aac tcc ctg aac gtc caa cgt gtc ctg acc ttt caa ccc cta cgc			870
Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe Gln Pro Leu Arg			
	265	270	275
ttc atc caa gaa cac gta ctg atc cct gtc ttg gac ctc agt ggc ccc			918
Phe Ile Gln Glu His Val Leu Ile Pro Val Leu Asp Leu Ser Gly Pro			
	280	285	290
agc agt ctg cct cag ccc atc cag tac tcc caa gtg gtg gtg tct ggg			966
Ser Ser Leu Pro Gln Pro Ile Gln Tyr Ser Gln Val Val Val Ser Gly			
	295	300	305
ccc agg gag cct cct gga gct gtg tgg cgg cag agc ctg tct gac ctc			1014
Pro Arg Glu Pro Pro Gly Ala Val Trp Arg Gln Ser Leu Ser Asp Leu			
	310	315	320
acc tac gta ggg cag tca gat gtc tcc atc ctg caa cct acc aac gtg			1062
Thr Tyr Val Gly Gln Ser Asp Val Ser Ile Leu Gln Pro Thr Asn Val			
	325	330	335
cca gct cag cag aca ctg tcc cca cca tcc tac gct ccg aag gct gtc			1110
Pro Ala Gln Gln Thr Leu Ser Pro Pro Ser Tyr Ala Pro Lys Ala Val			
	345	350	355
cct gag gtc cag ccc cct tcc tat gcg cct cag gta gcc tcg gat gcc			1158
Pro Glu Val Gln Pro Pro Ser Tyr Ala Pro Gln Val Ala Ser Asp Ala			
	360	365	370
aaa gct ctg ttc tac tca cca caa cag ggg atg aag acc agg cct gcc			1206
Lys Ala Leu Phe Tyr Ser Pro Gln Gln Gly Met Lys Thr Arg Pro Ala			
	375	380	385
acc tat gac ccg cag gac att ctg gac agc tgc cct gct tct tat gct			1254
Thr Tyr Asp Pro Gln Asp Ile Leu Asp Ser Cys Pro Ala Ser Tyr Ala			
	390	395	400

```

gtg tgt gtg gaa gac tct ggc aaa gac tct acc cca ggc atc ctc tcc 1302
Val Cys Val Glu Asp Ser Gly Lys Asp Ser Thr Pro Gly Ile Leu Ser
405                               410                               415                               420

act ccc aaa tac ctc aag aca aaa ggt cag ctc cag gaa gac aca ctt 1350
Thr Pro Lys Tyr Leu Lys Thr Lys Gly Gln Leu Gln Glu Asp Thr Leu
                               425                               430                               435

gtt aga agc tgt ctc cca ggg gac ctt tct cta cag aaa gtc acc tcc 1398
Val Arg Ser Cys Leu Pro Gly Asp Leu Ser Leu Gln Lys Val Thr Ser
                               440                               445                               450

tta ggt gaa ggg gag aca cag aga cca aaa tca ctc ccc tca cct ctg 1446
Leu Gly Glu Gly Glu Thr Gln Arg Pro Lys Ser Leu Pro Ser Pro Leu
                               455                               460                               465

gga ttt tgc aca gac aga gga cct gac ctt cac aca ctg cgc agt gag 1494
Gly Phe Cys Thr Asp Arg Gly Pro Asp Leu His Thr Leu Arg Ser Glu
                               470                               475                               480

gaa cca gag aca cca cgg tac ctg aag ggg gcg ctg tct ctc ctg tcc 1542
Glu Pro Glu Thr Pro Arg Tyr Leu Lys Gly Ala Leu Ser Leu Leu Ser
485                               490                               495                               500

tct gtg cag atc gag ggc cac cct gtc tcc ctc cct ttg cac gtc cat 1590
Ser Val Gln Ile Glu Gly His Pro Val Ser Leu Pro Leu His Val His
                               505                               510                               515

tct gtc tca tgt tcc ccc tca gac gag gga cca agt ccc tgg ggc ctg 1638
Ser Val Ser Cys Ser Pro Ser Asp Glu Gly Pro Ser Pro Trp Gly Leu
                               520                               525                               530

ctg gac tcc ctt gtg tgt cca aag gat gag ggt ccc gcg gtt gag act 1686
Leu Asp Ser Leu Val Cys Pro Lys Asp Glu Gly Pro Ala Val Glu Thr
                               535                               540                               545

gag gcc atg tgc ccc agt gct gca gcc tct gag ctg gag cag tcc aca 1734
Glu Ala Met Cys Pro Ser Ala Ala Ala Ser Glu Leu Glu Gln Ser Thr
                               550                               555                               560

gaa ctg gac tct ctt ttc aaa ggc ttg gcc ctg act gtg cag tgg gaa 1782
Glu Leu Asp Ser Leu Phe Lys Gly Leu Ala Leu Thr Val Gln Trp Glu
565                               570                               575                               580

tcc tga agggagatcg gagcaagcag gcctaagttt cctccccgcc caccta 1834
Ser *
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<210> 42
<211> 581
<212> PRT
<213> Mus musculus
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<400> 42
Met Lys Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
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Thr Thr Val Asp Thr Ser Gly Leu Leu Gln His Val Lys Phe Gln Ser
 20      25      30
Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Gly Gly Pro Ala Ser Thr
 35      40      45
Ser Asp Thr Val Tyr Ser Val Glu Tyr Lys Lys Tyr Gly Glu Arg Lys
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50		55		60											
Trp	Leu	Ala	Lys	Ala	Gly	Cys	Gln	Arg	Ile	Thr	Gln	Lys	Phe	Cys	Asn
65					70					75					80
Leu	Thr	Met	Glu	Thr	Arg	Asn	His	Thr	Glu	Phe	Tyr	Tyr	Ala	Lys	Val
				85					90					95	
Thr	Ala	Val	Ser	Ala	Gly	Gly	Pro	Pro	Val	Thr	Lys	Met	Thr	Asp	Arg
			100				105						110		
Phe	Ser	Ser	Leu	Gln	His	Thr	Thr	Ile	Lys	Pro	Pro	Asp	Val	Thr	Cys
		115					120					125			
Ile	Pro	Lys	Val	Arg	Ser	Ile	Gln	Met	Leu	Val	His	Pro	Thr	Leu	Thr
	130					135					140				
Pro	Val	Leu	Ser	Glu	Asp	Gly	His	Gln	Leu	Thr	Leu	Glu	Glu	Ile	Phe
145					150					155					160
His	Asp	Leu	Phe	Tyr	Arg	Leu	Glu	Leu	His	Val	Asn	His	Thr	Tyr	Gln
				165					170					175	
Met	His	Leu	Glu	Gly	Lys	Gln	Arg	Glu	Tyr	Glu	Phe	Leu	Gly	Leu	Thr
			180					185					190		
Pro	Asp	Thr	Glu	Phe	Leu	Gly	Ser	Ile	Thr	Ile	Leu	Thr	Pro	Ile	Leu
		195					200					205			
Ser	Lys	Glu	Ser	Ala	Pro	Tyr	Val	Cys	Arg	Val	Lys	Thr	Leu	Pro	Asp
	210					215					220				
Arg	Thr	Trp	Ala	Tyr	Ser	Phe	Ser	Gly	Ala	Val	Leu	Phe	Ser	Met	Gly
225					230					235					240
Phe	Leu	Val	Gly	Leu	Leu	Cys	Tyr	Leu	Gly	Tyr	Lys	Tyr	Ile	Thr	Lys
			245					250						255	
Pro	Pro	Val	Pro	Pro	Asn	Ser	Leu	Asn	Val	Gln	Arg	Val	Leu	Thr	Phe
			260					265					270		
Gln	Pro	Leu	Arg	Phe	Ile	Gln	Glu	His	Val	Leu	Ile	Pro	Val	Leu	Asp
	275						280					285			
Leu	Ser	Gly	Pro	Ser	Ser	Leu	Pro	Gln	Pro	Ile	Gln	Tyr	Ser	Gln	Val
	290					295					300				
Val	Val	Ser	Gly	Pro	Arg	Glu	Pro	Pro	Gly	Ala	Val	Trp	Arg	Gln	Ser
305					310					315					320
Leu	Ser	Asp	Leu	Thr	Tyr	Val	Gly	Gln	Ser	Asp	Val	Ser	Ile	Leu	Gln
			325					330					335		
Pro	Thr	Asn	Val	Pro	Ala	Gln	Gln	Thr	Leu	Ser	Pro	Pro	Ser	Tyr	Ala
			340					345					350		
Pro	Lys	Ala	Val	Pro	Glu	Val	Gln	Pro	Pro	Ser	Tyr	Ala	Pro	Gln	Val
		355					360					365			
Ala	Ser	Asp	Ala	Lys	Ala	Leu	Phe	Tyr	Ser	Pro	Gln	Gln	Gly	Met	Lys
	370					375					380				
Thr	Arg	Pro	Ala	Thr	Tyr	Asp	Pro	Gln	Asp	Ile	Leu	Asp	Ser	Cys	Pro
385					390					395					400
Ala	Ser	Tyr	Ala	Val	Cys	Val	Glu	Asp	Ser	Gly	Lys	Asp	Ser	Thr	Pro
			405					410						415	
Gly	Ile	Leu	Ser	Thr	Pro	Lys	Tyr	Leu	Lys	Thr	Lys	Gly	Gln	Leu	Gln
			420					425					430		
Glu	Asp	Thr	Leu	Val	Arg	Ser	Cys	Leu	Pro	Gly	Asp	Leu	Ser	Leu	Gln
		435					440					445			
Lys	Val	Thr	Ser	Leu	Gly	Glu	Gly	Glu	Thr	Gln	Arg	Pro	Lys	Ser	Leu
	450					455					460				
Pro	Ser	Pro	Leu	Gly	Phe	Cys	Thr	Asp	Arg	Gly	Pro	Asp	Leu	His	Thr
465					470					475					480
Leu	Arg	Ser	Glu	Glu	Pro	Glu	Thr	Pro	Arg	Tyr	Leu	Lys	Gly	Ala	Leu
			485					490						495	
Ser	Leu	Leu	Ser	Ser	Val	Gln	Ile	Glu	Gly	His	Pro	Val	Ser	Leu	Pro
			500					505					510		
Leu	His	Val	His	Ser	Val	Ser	Cys	Ser	Pro	Ser	Asp	Glu	Gly	Pro	Ser
		515					520					525			
Pro	Trp	Gly	Leu	Leu	Asp	Ser	Leu	Val	Cys	Pro	Lys	Asp	Glu	Gly	Pro
	530					535					540				
Ala	Val	Glu	Thr	Glu	Ala	Met	Cys	Pro	Ser	Ala	Ala	Ala	Ser	Glu	Leu

545 550 555 560
 Glu Gln Ser Thr Glu Leu Asp Ser Leu Phe Lys Gly Leu Ala Leu Thr
 565 570 575
 Val Gln Trp Glu Ser

<210> 43
 <211> 660
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> (1)...(660)

<400> 43
 atg gcg tgg agt ctt ggg agc tgg ctg ggt ggc tgc ctg ctg gtg tca 48
 Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
 1 5 10 15

gca ttg gga atg gta cca cct ccc gaa aat gtc aga atg aat tct gtt 96
 Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
 20 25 30

aat ttc aag aac att cta cag tgg gag tca cct gct ttt gcc aaa ggg 144
 Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
 35 40 45

aac ctg act ttc aca gct cag tac cta agt tat agg ata ttc caa gat 192
 Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
 50 55 60

aaa tgc atg aat act acc ttg acg gaa tgt gat ttc tca agt ctt tcc 240
 Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
 65 70 75 80

aag tat ggt gac cac acc ttg aga gtc agg gct gaa ttt gca gat gag 288
 Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
 85 90 95

cat tca gac tgg gta aac atc acc ttc tgt cct gtg gat gac acc att 336
 His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
 100 105 110

att gga ccc cct gga atg caa gta gaa gta ctt gat gat tct tta cat 384
 Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
 115 120 125

atg cgt ttc tta gcc cct aaa att gag aat gaa tac gaa act tgg act 432
 Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
 130 135 140

atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa 480
 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
 145 150 155 160

aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag 528
 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
 165 170 175

gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga 576

Val	Leu	Arg	Asn	Leu	Glu	Pro	Trp	Thr	Thr	Tyr	Cys	Val	Gln	Val	Arg		
			180					185					190				
ggg	ttt	ctt	cct	gat	cgg	aac	aaa	gct	ggg	gaa	tgg	agt	gag	cct	gtc	624	
Gly	Phe	Leu	Pro	Asp	Arg	Asn	Lys	Ala	Gly	Glu	Trp	Ser	Glu	Pro	Val		
		195					200					205					
tgt	gag	caa	aca	acc	cat	gac	gaa	acg	gtc	ccc	tcc					660	
Cys	Glu	Gln	Thr	Thr	His	Asp	Glu	Thr	Val	Pro	Ser						
	210					215					220						

<210> 44
 <211> 220
 <212> PRT
 <213> Homo Sapiens

<400> 44																	
Met	Ala	Trp	Ser	Leu	Gly	Ser	Trp	Leu	Gly	Gly	Cys	Leu	Leu	Val	Ser		
1				5					10					15			
Ala	Leu	Gly	Met	Val	Pro	Pro	Pro	Glu	Asn	Val	Arg	Met	Asn	Ser	Val		
			20					25					30				
Asn	Phe	Lys	Asn	Ile	Leu	Gln	Trp	Glu	Ser	Pro	Ala	Phe	Ala	Lys	Gly		
		35					40					45					
Asn	Leu	Thr	Phe	Thr	Ala	Gln	Tyr	Leu	Ser	Tyr	Arg	Ile	Phe	Gln	Asp		
	50					55					60						
Lys	Cys	Met	Asn	Thr	Thr	Leu	Thr	Glu	Cys	Asp	Phe	Ser	Ser	Leu	Ser		
	65				70					75				80			
Lys	Tyr	Gly	Asp	His	Thr	Leu	Arg	Val	Arg	Ala	Glu	Phe	Ala	Asp	Glu		
			85						90					95			
His	Ser	Asp	Trp	Val	Asn	Ile	Thr	Phe	Cys	Pro	Val	Asp	Asp	Thr	Ile		
			100					105					110				
Ile	Gly	Pro	Pro	Gly	Met	Gln	Val	Glu	Val	Leu	Asp	Asp	Ser	Leu	His		
		115				120						125					
Met	Arg	Phe	Leu	Ala	Pro	Lys	Ile	Glu	Asn	Glu	Tyr	Glu	Thr	Trp	Thr		
	130					135					140						
Met	Lys	Asn	Val	Tyr	Asn	Ser	Trp	Thr	Tyr	Asn	Val	Gln	Tyr	Trp	Lys		
	145				150					155				160			
Asn	Gly	Thr	Asp	Glu	Lys	Phe	Gln	Ile	Thr	Pro	Gln	Tyr	Asp	Phe	Glu		
			165					170					175				
Val	Leu	Arg	Asn	Leu	Glu	Pro	Trp	Thr	Thr	Tyr	Cys	Val	Gln	Val	Arg		
			180					185					190				
Gly	Phe	Leu	Pro	Asp	Arg	Asn	Lys	Ala	Gly	Glu	Trp	Ser	Glu	Pro	Val		
		195				200						205					
Cys	Glu	Gln	Thr	Thr	His	Asp	Glu	Thr	Val	Pro	Ser						
	210					215					220						

<210> 45
 <211> 199
 <212> PRT
 <213> homo sapiens

<400> 45																	
Met	Val	Pro	Pro	Pro	Glu	Asn	Val	Arg	Met	Asn	Ser	Val	Asn	Phe	Lys		
1				5					10					15			
Asn	Ile	Leu	Gln	Trp	Glu	Ser	Pro	Ala	Phe	Ala	Lys	Gly	Asn	Leu	Thr		
			20					25					30				
Phe	Thr	Ala	Gln	Tyr	Leu	Ser	Tyr	Arg	Ile	Phe	Gln	Asp	Lys	Cys	Met		
		35					40					45					
Asn	Thr	Thr	Leu	Thr	Glu	Cys	Asp	Phe	Ser	Ser	Leu	Ser	Lys	Tyr	Gly		
	50					55					60						

```

Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu His Ser Asp
65      70      75      80
Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile Ile Gly Pro
      85      90      95
Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His Met Arg Phe
      100      105      110
Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn
      115      120      125
Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys Asn Gly Thr
      130      135      140
Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg
145      150      155      160
Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu
      165      170      175
Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln
      180      185      190
Thr Thr His Asp Glu Thr Val
      195

```

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<210> 46
<211> 211
<212> PRT
<213> Homo sapiens

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```

<400> 46
Ser Asp Ala His Gly Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe
1      5      10      15
Glu Ala Glu Phe Phe His His Ile Leu His Trp Thr Pro Ile Pro Asn
      20      25      30
Gln Ser Glu Ser Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile
      35      40      45
Glu Ser Trp Asn Ser Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp
      50      55      60
Leu Thr Ala Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala
65      70      75      80
Arg Val Arg Ala Val Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr
      85      90      95
Asn Thr Arg Phe Ser Val Asp Glu Val Thr Leu Thr Val Gly Ser Val
      100      105      110
Asn Leu Glu Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro
      115      120      125
Arg Pro Lys Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser
      130      135      140
His Phe Arg Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe
145      150      155      160
Thr Phe Thr His Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr
      165      170      175
Ser Gly Glu Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala
      180      185      190
Ser Arg Ser Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu
      195      200      205
Thr Arg Gln
      210

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<210> 47
<211> 201
<212> PRT
<213> homo sapiens

```

```

<400> 47

```

```

Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
 1          5          10          15
Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly
          20          25          30
Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu
          35          40          45
Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu
          50          55          60
Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr
65          70          75          80
Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser
          85          90          95
Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro
          100          105          110
Gly Met Glu Ile Thr Lys Asp Gly Phe His Leu Val Ile Glu Leu Glu
          115          120          125
Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Arg Arg Glu
          130          135          140
Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro
145          150          155          160
Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala
          165          170          175
Gln Thr Phe Val Lys Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr
          180          185          190
Glu Cys Val Glu Val Gln Gly Glu Ala
          195          200

```

```

<210> 48
<211> 68
<212> PRT
<213> Mus musculus

```

```

<400> 48
His Thr Thr Val Asp Thr Ser Gly Leu Leu Gln His Val Lys Phe Gln
 1          5          10          15
Ser Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Gly Gly Pro Ala Ser
          20          25          30
Thr Ser Asp Thr Val Tyr Ser Val Glu Tyr Lys Lys Tyr Gly Glu Arg
          35          40          45
Lys Trp Leu Ala Lys Ala Gly Cys Gln Arg Ile Thr Gln Lys Phe Cys
          50          55          60
Asn Leu Thr Met
65

```

```

<210> 49
<211> 26
<212> PRT
<213> mus musculus

```

```

<400> 49
Glu Thr Arg Asn His Thr Glu Phe Tyr Tyr Ala Lys Val Thr Ala Val
 1          5          10          15
Ser Ala Gly Gly Pro Pro Val Thr Lys Met
          20          25

```

```

<210> 50
<211> 28
<212> PRT
<213> mus musculus

```

<400> 50

Thr	Asp	Arg	Phe	Ser	Ser	Leu	Gln	His	Thr	Thr	Ile	Lys	Pro	Pro	Asp
1				5					10					15	
Val	Thr	Cys	Ile	Pro	Lys	Val	Arg	Ser	Ile	Gln	Met				
			20					25							

<210> 51

<211> 40

<212> PRT

<213> Mus musculus

<400> 51

Leu	Val	His	Pro	Thr	Leu	Thr	Pro	Val	Leu	Ser	Glu	Asp	Gly	His	Gln
1				5					10					15	
Leu	Thr	Leu	Glu	Glu	Ile	Phe	His	Asp	Leu	Phe	Tyr	Arg	Leu	Glu	Leu
			20					25					30		
His	Val	Asn	His	Thr	Tyr	Gln	Met								
		35					40								

<210> 52

<211> 50

<212> PRT

<213> Mus musculus

<400> 52

His	Leu	Glu	Gly	Lys	Gln	Arg	Glu	Tyr	Glu	Phe	Leu	Gly	Leu	Thr	Pro
1				5					10					15	
Asp	Thr	Glu	Phe	Leu	Gly	Ser	Ile	Thr	Ile	Leu	Thr	Pro	Ile	Leu	Ser
			20					25					30		
Lys	Glu	Ser	Ala	Pro	Tyr	Val	Cys	Arg	Val	Lys	Thr	Leu	Pro	Leu	Val
		35					40					45			
Pro	Arg														
	50														

<210> 53

<211> 70

<212> PRT

<213> Mus musculus

<400> 53

His	Leu	Glu	Gly	Lys	Gln	Arg	Glu	Tyr	Glu	Phe	Leu	Gly	Leu	Thr	Pro
1				5					10					15	
Asp	Thr	Glu	Phe	His	Leu	Glu	Gly	Lys	Gln	Arg	Glu	Tyr	Glu	Phe	Leu
			20					25					30		
Gly	Leu	Thr	Pro	Asp	Thr	Glu	Phe	Leu	Gly	Ser	Ile	Thr	Ile	Leu	Thr
		35					40					45			
Pro	Ile	Leu	Ser	Lys	Glu	Ser	Ala	Pro	Tyr	Val	Cys	Arg	Val	Lys	Thr
	50					55					60				
Leu	Pro	Leu	Val	Pro	Arg										
65					70										

<210> 54

<211> 46

<212> PRT

<213> Mus musculus

<400> 54

Glu	Thr	Arg	Asn	His	Thr	Glu	Phe	Tyr	Tyr	Ala	Lys	Val	Thr	Ala	Val
1				5					10					15	
Ser	Ala	Gly	Gly	Glu	Thr	Arg	Asn	His	Thr	Glu	Phe	Tyr	Tyr	Ala	Lys
		20					25						30		
Val	Thr	Ala	Val	Ser	Ala	Gly	Gly	Pro	Pro	Val	Thr	Lys	Met		
	35					40						45			

<210> 55
 <211> 48
 <212> PRT
 <213> mus musculus

<220>
 <221> VARIANT
 <222> 6, 11, 13,
 <223> Xaa = Any Amino Acid

Thr	Asp	Arg	Phe	Ser	Xaa	Leu	Gln	His	Thr	Xaa	Ile	Xaa	Pro	Xaa	Asp
1				5					10					15	
Xaa	Xaa	Xaa	Ile	Thr	Asp	Arg	Phe	Ser	Ser	Leu	Gln	His	Thr	Thr	Ile
		20					25						30		
Lys	Pro	Pro	Asp	Val	Thr	Cys	Ile	Pro	Lys	Val	Arg	Ser	Ile	Gln	Met
	35					40						45			

<210> 56
 <211> 92
 <212> PRT
 <213> homo sapiens

Pro	Glu	Asp	Pro	Ser	Asp	Leu	Leu	Gln	His	Val	Lys	Phe	Gln	Ser	Ser
1				5					10					15	
Asn	Phe	Glu	Asn	Ile	Leu	Thr	Trp	Asp	Ser	Gly	Pro	Glu	Gly	Thr	Pro
		20					25						30		
Asp	Thr	Val	Tyr	Ser	Ile	Glu	Tyr	Lys	Thr	Tyr	Gly	Glu	Arg	Asp	Trp
	35					40					45				
Val	Ala	Lys	Lys	Gly	Cys	Gln	Arg	Ile	Thr	Arg	Lys	Ser	Cys	Asn	Leu
	50				55					60					
Thr	Val	Glu	Thr	Gly	Asn	Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val	Thr
65					70				75					80	
Ala	Val	Ser	Ala	Gly	Gly	Arg	Ser	Ala	Thr	Lys	Met				
			85					90							

<210> 57
 <211> 28
 <212> PRT
 <213> Homo sapiens

Thr	Asp	Arg	Phe	Ser	Ser	Leu	Gln	His	Thr	Thr	Leu	Lys	Pro	Pro	Asp
1				5					10					15	
Val	Thr	Cys	Ile	Ser	Lys	Val	Arg	Ser	Ile	Gln	Met				
		20					25								

<210> 58
 <211> 40
 <212> PRT

<213> Homo sapiens

<400> 58

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Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly His Arg
 1              5              10              15
Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu Glu Leu
              20              25              30
Gln Val Asn Arg Thr Tyr Gln Met
              35              40

```

<210> 59

<211> 25

<212> PRT

<213> Homo sapiens

<400> 59

```

His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro
 1              5              10              15
Asp Thr Glu Phe Leu Gly Thr Ile Met
              20              25

```

<210> 60

<211> 14

<212> PRT

<213> Homo sapiens

<400> 60

```

Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr Met
 1              5              10

```

<210> 61

<211> 12

<212> PRT

<213> Homo sapiens

<400> 61

```

Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Thr
 1              5              10

```

<210> 62

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> A murine IL-22RA soluble receptor with cleavage
site (Leu Val Pro Arg) remaining on C-Terminus

<400> 62

```

His Thr Thr Val Asp Thr Ser Gly Leu Leu Gln His Val Lys Phe Gln
 1              5              10              15
Ser Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Gly Gly Pro Ala Ser
              20              25              30
Thr Ser Asp Thr Val Tyr Ser Val Glu Tyr Lys Lys Tyr Gly Glu Arg
              35              40              45
Lys Trp Leu Ala Lys Ala Gly Cys Gln Arg Ile Thr Gln Lys Phe Cys
              50              55              60
Asn Leu Thr Met Glu Thr Arg Asn His Thr Glu Phe Tyr Tyr Ala Lys

```

[illegible]